

SEQUENCE LISTING

<110> Moore et al.

<120> Human Transcription Factor IIA

<130> PF135D2

<150> PCT/US94/10644

<151> 1994-09-20

<150> US 08/411,635

<151> 1995-04-11

<150> US 08/845,011

<151> 1997-04-22

<160> 5

<170> PatentIn version 3.1

<210> 1

<211> 804

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (190)..(519)

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gtgggtcggag aagtaggaac ctctgccgg gctcgtggcg gcttctgtcc gtcgccgga 120

gggaagcgcc tccccacag gacatcaatg caagcttgaa taagaaaaac aaattcttcc 180

tcctaagcc atg gca tat cag tta tac aga aat act act ttg gga aac agt 231

Met Ala Tyr Gln Leu Tyr Arg Asn Thr Thr Leu Gly Asn Ser

1 5 10

ctt cag gag agc cta gat gag ctc ata cag tct caa cag atc acc ccc 279

Leu Gln Glu Ser Leu Asp Glu Leu Ile Gln Ser Gln Gln Ile Thr Pro

15 20 25 30

caa ctt gcc ctt caa gtt cta ctt cag ttt gat aag gct ata aat gca 327

Gln Leu Ala Leu Gln Val Leu Leu Gln Phe Asp Lys Ala Ile Asn Ala

35 40 45

gca ctg gct cag agg gtc agg aac aga gtc aat ttc agg ggc tct cta 375

Ala Leu Ala Gln Arg Val Arg Asn Arg Val Asn Phe Arg Gly Ser Leu

50 55 60

aat acg tac aga ttc tgc gat aat gtg tgg act ttt gta ctg aat gat 423

Asn Thr Tyr Arg Phe Cys Asp Asn Val Trp Thr Phe Val Leu Asn Asp

65 70 75

gtt gaa ttc aga gag gtg aca gaa ctt att aaa gtg gat aaa gtg aaa 471
Val Glu Phe Arg Glu Val Thr Glu Leu Ile Lys Val Asp Lys Val Lys
80 85 90

att gta gcc tgt gat ggt aaa aat act ggc tcc aat act aca gaa tga 519
Ile Val Ala Cys Asp Gly Lys Asn Thr Gly Ser Asn Thr Thr Glu
95 100 105

atagaaaaaa tatgactttt ttacaccatc ttctgttatt cattgctttt gaagagaagc 579

atagaagaga ctttttattt attctagaat tgcagaaatg actacactgt gctaraccag 639

agaattccag tagaaagaaa cttgtaactc tctagcctct tacatcacct ttattatata 699

gcatgaaaaa ccataacttt tttttaagga caaaagtgtg tgccttccta agaaccttct 759

ttaataaaact catttttaaaa ctctgaaaaa aaaaaaaaaa aaaaa 804

<210> 2
<211> 109
<212> PRT
<213> Homo sapiens

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Met Ala Tyr Gln Leu Tyr Arg Asn Thr Thr Leu Gly Asn Ser Leu Gln
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Glu Ser Leu Asp Glu Leu Ile Gln Ser Gln Gln Ile Thr Pro Gln Leu
20 25 30

Ala Leu Gln Val Leu Leu Gln Phe Asp Lys Ala Ile Asn Ala Ala Leu
35 40 45

Ala Gln Arg Val Arg Asn Arg Val Asn Phe Arg Gly Ser Leu Asn Thr
50 55 60

Tyr Arg Phe Cys Asp Asn Val Trp Thr Phe Val Leu Asn Asp Val Glu
65 70 75 80

Phe Arg Glu Val Thr Glu Leu Ile Lys Val Asp Lys Val Lys Ile Val
85 90 95

Ala Cys Asp Gly Lys Asn Thr Gly Ser Asn Thr Thr Glu
100 105

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<211> 29
<212> DNA
<213> Artificial sequence

<220>
 <223> Contains a Bam HI restriction enzyme site

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 <211> 26
 <212> DNA
 <213> Artificial sequence

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 <223> Contains complementary sequences to a HindIII site

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 <211> 121
 <212> PRT
 <213> *Saccharomyces cerevisiae*

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 1 5 10 15

 Asn Ser Leu Val Asp Ala Leu Asp Thr Leu Ile Ser Asp Gly Arg Ile
 20 25 30

 Glu Ala Ser Leu Ala Met Arg Val Leu Glu Thr Phe Asp Lys Val Val
 35 40 45

 Ala Glu Thr Leu Lys Asp Asn Thr Gln Ser Lys Leu Thr Val Lys Gly
 50 55 60

 Asn Leu Asp Thr Tyr Gly Phe Cys Asp Asp Val Trp Thr Phe Ile Val
 65 70 75 80

 Lys Asn Cys Gln Val Thr Val Glu Asp Ser His Arg Asp Ala Ser Gln
 85 90 95

 Asn Gly Ser Gly Asp Ser Ser Val Ile Ser Val Asp Lys Leu Arg Ile
 100 105 110

 Val Ala Cys Asn Ser Lys Lys Ser Glu
 115 120